USSN: 09/405,940 Exhibit A

Docket No.: PF-0346-2 CPA

1 - 200

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BLAST2 Search Results

Translation Phrap ClustalW 606 Assembly FASTA BLAST2 BLAST 2 Manu Retrieval

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Program: blastp

Sequence ID(s):

983910CD1 vs. <u>genpept136</u>

NCBI-BLASTP 2.0.10 [Aug-26-1999]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghul Zhang, Zheng Thang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:1389-3402.

Query= 983910CD1

(314 letters)

Database: genpept136

1,453,555 sequences; 449,659,834 total letters

.....done Searching

e-154 e-147 e-137 e-137 550 e-155 Score E (bits) Value 546 522 490 490 F 433912 T-cell receptor F 433912 T-cell receptor product (unidentified)
F 42469288 T cell receptor beta chain BV1251 J1-1 BC1 [Homo sa g3002935 T cell receptor beta chain [Homo sapiens] T-cell receptor beta [Homo sapiens] Sequences producing significant alignments: 91100182

Score = 550 bits (1401), Expect = e-155 Identities = 272/311 (87%), Positives = 280/311 (89%), Gaps = 3/311 (0%)

Query: 1 MOTRILCWAALCLIGADHTCACVSCYTPSNRVTEXGEDVELRCDP1SGHTALWYRGSLGQ 60
MOTRIL W A CLICADHTCACVSCY-PSNRVTEXGEDVELRCDP1SGHTALWYRGSLGQ
Sbjct: 1 MOTRILLPWYAFCLIGADHTCAGVSCSPSNRVTEXGKDVELRCDP1SGHTALWYRGSLGQ 60

http://patents.incyte.com:8000/cgi-bin/SeqServer/SeqServer

GPEFLIYFQGTGAADDSGLMDRFFAVRPEGSVSTIKIQRTBQGDSAAYLRAGVAAGMSS 120 G EFLIYFQG A D SGLP+DRF A R GSVSTL IQRT+Q DSA YL A+ S GLEFLIYFQGNSAPDKSGLPSDRFSAERTGGSVSTL/TIQRTQQEDSAVYL---CASSLSL 117 Sbjct: 61 Query: 61

Query: 121 YNEQYFGFGTRLITVLEDLKNVFPPEVAVFEPSEAEISHTQKATLVCLATGFYPDHVELSW 180

Sbjet: 118 LSPLAFCANSTRLIVTEDLAKVFPPEVAVFEPSEABISHTQKATLVCLATGIFPDHVELSM 177 +FG GTRLTV EDL VFPPEVAVFEPSEAEISHTQKATLVCLATG +PDHVELSW

Query: 181 WINGKEVHSGVSTDPQPIABQPALADSRYCLSSRLAVSATFWQNPRNFFRFFRCQVQFYGLSE 240 WINGKEVHSGVSTDPQPIADSRYCLSSRLAVSATFWGNFRNFFRFFRCQVQFYGLSE Sbjet: 178 WVNGKEVHSGVSTDPQPLKEQPALNDSRYCLSSRLRVSATFWQNPRNHFRCQVQFYGLSE 237

Query: 241 NDEWTQDRAKFVTQTVSAEAWGRADCGFTSESYQQGVLSATILYEILLGKATLYAVLVSA 300 NDEWTODRAKEVTOIVSAEAMGRADCGFTS SYQQGVLSATILYELLLGKAT+YAVLVSA Sbjct: 238 NDEWTODRAKEVTOIVSAEAMGRADCGFTSVSYQQGVLSATILYELLLGKATMYAVLVSA 297

Query: 301 LVLMAMVRRKD 311

LVIAMAMVKRKD Sbjct: 298 LVIAMAMVKRKD 308

>q1100182 T-cell receptor beta [Homo sapiens]

Length = 311

+

Score = 546 bits (1391), Expect = e-154 Identities = 268/314 (85%), Positives = 282/314 (89%), Gaps = 3/314 (0%)

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Query: 1 MGTRLLCWAALCLLGADHTGAGVSQTPSNKVTEKGKDVELRCDPISGHTALYWYRQSLGQ 60

MGT LLCM ALCLIGADH GVSQ P +K+T++G++V RCDPIS H LYWYRQ+LQQ SDjct: 1 MGTSLLGWALCLIGADHADTGVSQNFRHKLTRRGQNVTFRCDPISEJRRLYWYRQTLQQ 60

GPEFLIYFQCTGAADDSGLPNDRFFAVRPEGSVSTLKIQRTEQGDSAAYLRAGVAAGWSS 120 Query: 61

GPET. YPQ + S L. +DNF A RP+GS STL-1QKTEQCOSA YL A ++ +S Sbjct: 61 GPEFLYYPQNEAQLEKSRLASDRFSARRFKGSPSTLEIQKTEQCDSAWYLCA--SSPOTS 118

Query: 121 YNEQYFGFGTRLTVLEDLKNVFPPEVAVFEPSEAEISHTQKATLVCLATGFYFDHVELSW 180

Y BQYPGPOTRUTV EDLKNVPPPENAVFEPSBAEISHTQKATLNCLATGFYPDHVZLSM Sbjct: 119 Y-BQYPGPOTRUTVTEDLKNVPPPENAVFEPSBAEISHTQKATLNCLATGFYPDHYZLSM 177

Query: 181 WVNGKEVHSGVSTDPQPLKEQPALADSRYCLSSRLRVSATFWQNFRNHFRCQVQFYGLSE 240 WVNGKEVHSGVSTIDPQPLKEQPALAIDSRYCLSSRLRVSATFWQNPRAHFRCQVQFYGLSE

Sbjct: 178 WVNGKEVHSGVSTDPQPLKEQPALADSRYCLSSRLRVSATFWQNPRNHFRCQVQFYGLSE 237

Query: 241 NDEWTQDRAKFVTQIVSAEAMGRADCGFTSESYQQGVLSATILYEILLGKATLYAVIJVSA 300 NDEWTORAKFVTOTVSABAWSRADCGFTSESYQQSVISATILYETILLGKATIANTAVSA Sbjet: 238 NDEWTORAKFVTQIVSABAMGRADCGFTSESYQQGVISATILYETILLGKATIANUVSA 297

Query: 301 IVLMAMVRRKDSRG 314 IVLMAMVRRKDSRG

Sbjct: 298 LVLMAMVKRKDSRG 311

>q339012 T-cell receptor precursor [Homo sapiens]

Score = 522 bits (1330), Expect = e-147 Identities = 254/311 (81%), Positives = 271/311 (86%), Gaps = 2/311 (0%)

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Query: 181 WYMGKEWHSGVSTDRQPLKEQPALADSRYCLSSRLRVSATFWQMPRNHFRCQVQPYGLSE 240 WYMGKEWHSGVSTDRQPLKEQPALADSRYCLSSRLRVSATFWQMPRUHPRCQVQPYGLSE
                                                                                                                                                                                                                                                                                                                                              G E LIYF DDSGAP DRP A P S STAKIQ 4E DSA Y A+ ++
Sbjct: 61 GLELLIYFWRANVPIDDSGAPEDRESANFRWASPSTIKIQPSEROSANYF--CASSENG 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query: 121 YNEQYFGFGTRLIVLEDLKNVFPPEVAVFEPSEAEISHTQKATLVCLATGFYPDHVELSW 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E +PG GTRLIV+EDL VPPPEVAVPEPSEAEISHTQKATLVCLATGF+PDHVELSM SDjct: 118 AGGAFPGQGTRLIVVEDIAKVPPPEVAVFEPSEAEISHTQKATLVCLATGFPDHVELSW 177
                                                                                                                                                                                                                                                                                                            GPEFLIYFQGTGAADDSGLPNDRFFAVRPEGSVSTLKIQRTEQGDSAAYLRAGVAAGWSS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sbjct: 178 WYNGKEVHSGVSTDPOPLKEOPALADSRYCLSSRLRVSATFWONPRNHFRCQVQFYGLSE 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query: 241 NDEWTQDRAKFVTQIVSAEAWGRADCGFTSESYQQGVLSATILYEILLGKATLYAVLVSA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NDBATQDRAKPVTQIVSAEAMGRADCGFTS SYQQGVLSATILYEILLGKATLYAVLVSA
Sbjct: 238 NDBATQDRAKPVTQIVSAEAMGRADCGFTSVSYQQGVLSATILYEILLGKATLYAVLVSA 297
                                                                                                                                                                           M + C +LC+L A HT AGV Q+P ++VTB G++V LRC PISGH +L+WYRQ++ +
MDSWTPCCVSLCILVAKHTDAGVIQSPRHEVTERGQEVTLRCKPISGHNSLFWYRQTMRR 60
                                                                                                                                     Query: 1 MCTRLLCWAALCLLGADHTGAGVSQTPSNKVTTEKGKDVELRCDPISGHTALYWYRQSLGQ 60
                                               Identities = 241/311 (77%), Positives = 262/311 (83%), Gaps = 3/311 (0%)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Number of HSP's better than 10.0 without gapping: 4379
Number of HSP's better than 10.0 without gapping: 4379
Number of HSP's that attempted gapping in prelim test: 13046
Number of HSP's gapped (non-prelim): 19060
Mumber of query: 314
length of database: 449,659,834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Number of sequences in database: 1,453,555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Posted date: Jul 31, 2003 9:27 AM Number of letters in database: 449,659,834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Hits to DB: 297167763
Number of Sequences: 455355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Number of sequences better than 10.0: 17425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              effective length of query: 258
effective length of database: 568,260,754
effective search space: 95011274532
effective search space used: 95011274532
         Score = 490 bits (1249), Expect = e-137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Number of extensions: 12787980
Number of successful extensions: 59096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query: 301 LVLMAMVKRKD 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sbjct: 298 LVLMAMVKRKD 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     K H 0.133 0.411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             effective HSP length: 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Database: genpept136
Posted date: Jul 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LVLMAMVKRKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gapped
Lambda K H
0.270 0.0470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.318
                                                                                                                                                                                                                                                                                                                 Query: 61
                                                                                                                                                                                                                           Sbjct: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lambda
                                                                                                                                                                       GPEPLIYPQOYGAADDSGLRNDRFPAVRPBGSSVSTIÆIQRTBQGDSAAYIRAGVAAGMSS 120 GPEPL YFQ + S L +DRF A RP+GS STL+IQRTBQCDSA YL A \, AG +
                                                                                                                                                                                                                                                                                                                                                  Query: 121 YNDQYFGFOTRLIVLEDLANVFPPEVANFEPSEAEISHTQKATLVCLATGFYFDHVELSW 180
Q+FG GTRL++LEDL VFPEVANFEPSEAEISHTQKATLVCLATG +PDHVELSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query: 181 WANGKEVHSGVSTDPQPLKEQPALADSRYCLSSRLRVSATFWQNPRAHFRQQVQPYGLSE 240
WANGKEVHSGVSTDPQPLKEQPALADSRYCLSSRLRVSATFWQNPRAHFRCQVQPYGLSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query: 61 GPETLIYPQSTGAADDSGLFNDRPFAVRPBGSVSTLKIQRTEQGDSAAYLAAGWSS 120 EFL+ F + S + +D+F RE+GS TLKI+ T+ DSA Y A ++ +S
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sbjet: 121 --PQHFGDGTRLSILEDLAKVFPFEVAVFBPSEABISHTQKATLVCLATGIFPDHVELSW 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sbjet: 179 WVNGKEVHSGVSTDPQPLKEQPALADSRYCLSSRLRVSATFWQNPRNHFRCQVQFYGLSE 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NDEWTQDRAKPVTQIVSAEAWGRADCGFTS SYQQGVLSATILYEILLGRAT+YAVLVSA Sbjct: 239 NDEWTQDRAKPVTQIVSAEAWGRADCGFTSVSYQQGVLSATILYEILLGRATMYAVLVSA 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sbjet: 61 KVEFLVSFYNNEISEKSEIFDDQFSVERPDGSNFYLKIRSTKLEDSAMYFCA--SSETNS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query: 121 YNEQYFGPGTRLITVLEDLKNVFPPEVAVFEPSEAEISHTQKATLVCLATGFYPDHVELSW 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Y BQYFGFGTRLIV EDLKOVFPPEVANFEPSEAEISHTQKATLVCLATGFYFDHVELSM
Sbjct: 119 Y-EQYFGFGTRLIVYEDEDKAVFPPEVANFEPSEAEISHTQKATLVCLATGFYFDHVELSM 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query: 181 WVNEXEVHSGVSTDPQPLKEQPALADSRYCLSSRLRVSATFWQNPRNHFRCQVQFYGLSE 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NDBATQDRAKPUTQIVSABAMGRADCGFTSESYQGOTJSATILJVELLIJGRATLYAVIJVSA
Sbjet: 238 NDBATQDRAKPVTQIVSABAMGRADCGFTSESYQGOTJSATILJVELLIJGRATLYAVIJVSA 297
                                                                                                                                                                                                                                                                 GPEFLIYFQNEAQLEKSRLLSDRFSAERPKGSFSTLEIQRTEQGDSAMYLCASSLAGLNQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query: 241 NDEWTQDRAKFVTQIVSAEAMGRADCGFTSESYQQGVLSATILYEILLGKATLYAVLVSA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sbjct: 178 WVNEXEVHSGVSTDPQPLKEQPALNDSRYCLSSRLRVSATFWQNFRNHFRCQVQFYGLSE 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query: 241 NDEWIQDRAKPVTQIVSAEAWGRADCGFTSESYQQGVLSATILYBILLGKATLYAVLVSA 300
                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quesy: 1 MGTRILCMAALCLIGADHTGAGVSGTSSNRVTEKGEUVELRCDPISGSTALWWRQSLGQ 60
MT L-CWA LA A T V-VGTPS-NTV 6-+V LEC PIS H WYRQ LO
SPJCE: 1 MDWINGARISELLKAGLTREPENTOPRSSHQNTQWQSPILLREVPRISHLYWWRQLLGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score = 490 bits (1249), Expect = e-137
Identities = 248/314 (78%), Positives = 267/314 (84%), Gaps = 3/314 (0%)
MSTRLLCMAALCLIGADHTGACUSQTPSRKVTFKKUVELACDPISGHTALWAYRQSIGQ
MGT LLCM ALCLIGADH GUSQ P + 47+46+4V RCDPIS H LYWIRQ+LQQ
MGTSLLCMMALCLLGADHADTGUSQNPRHNITFKQQNVTFRCDPISGHNRLYWYRQTIGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WVNCKEVHSGVSTDPQPLKEQPALADSRYCLSSRLRVSATFWQNPRNHFRCQVQFYGLSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    >922469288 T cell receptor beta chain BV12S1 J1-1 BC1 [Homo sapiens]
Length = 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2g6741519 unnamed protein product (unidentified)
Length = 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query: 301 LVIMAMVKRKDSRG 314
LVIMAMVKRKDSRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sbjct: 298 LVLMAMVKRKDSRG 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query: 301 LVLMAMVRRKD 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sbjct: 299 LVLMAMVKRKD 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LVLMAMVKRKD
                                                                                                                                                                                Query: 61
                                                                                                                                                                                                                                                                      Sbjct: 61
         Query: 1
                                                                                     Sbjct: 1
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4 of 5

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T: 11 A: 40 XI: 16 (7.3 bits) XI: 38 (14.8 bits) XI: 64 (24.9 bits) SI: 41 (21.7 bits)

Submit sequences to: BLAST2 E Submit Reset

IncyteGenomics

8/28/03 9:56 AM